

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:

November 3, 2005, 08:19:03 ; Search time 181 seconds

(without alignments)

Title: US-10-628-432-32

Perfect score: 2859

Sequence: 1 MSQGSHPGRGLAGRWLWGA.....DQLQDPNIPQAVDYKDDDK 529

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result

No. Score Query

Match Length DB ID

Description

Result No.	Score	Match	Length	DB	ID	Description
1	2805	98.1	837	1	AT\$4_HUMAN	AT\$4_HUMAN STANDARD; PRT; 837 AA.
2	2798	97.9	837	2	Q6UWA8	ID: AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
3	2790	97.6	837	2	Q6P4Q8	AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
4	2557	89.4	839	2	Q7Y9S9	AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
5	2460	86.0	845	2	QBBN92	AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
6	2459	86.0	833	2	Q8K384	AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
7	2248	78.6	893	2	Q6A017	AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
8	1659	58.0	339	2	Q8NEK2	AT\$4_HUMAN; AC: Q75173; Q9JUN83; PRT; 837 AA.
9	1613	56.4	143	1	AT\$4_RAT	AT\$4_RAT; AC: Q7Y9S9; PRT; 143 AA.
10	1222	42.7	968	1	AT\$1_MOUSE	AT\$1_MOUSE; AC: Q9E977; PRT; 968 AA.
11	1221.5	42.7	967	1	AT\$1_RAT	AT\$1_RAT; AC: Q9E977; PRT; 968 AA.
12	1220.5	42.7	957	2	Q6BET2	AT\$1_RAT; AC: Q9E977; PRT; 968 AA.
13	1193	41.7	967	1	AT\$1_HUMAN	AT\$1_HUMAN; AC: Q9E977; PRT; 968 AA.
14	1193	41.7	967	2	QBNZ6	AT\$1_HUMAN; AC: Q9E977; PRT; 968 AA.
15	1108	38.8	245	1	AT\$4_BOVIN	AT\$4_BOVIN; AC: Q9E977; PRT; 245 AA.
16	1095	38.3	950	1	AT\$1_MOUSE	AT\$1_MOUSE; AC: Q9E977; PRT; 950 AA.
17	1084	37.9	203	2	Q8CBH0	AT\$1_MOUSE; AC: Q9E977; PRT; 203 AA.
18	1061	37.1	912	2	Q95M24	AT\$1_MOUSE; AC: Q9E977; PRT; 912 AA.
19	1053.5	36.8	890	1	AT\$2_HUMAN	AT\$2_HUMAN; AC: Q9E977; PRT; 890 AA.
20	1049.5	36.7	759	2	Q8HMB	AT\$2_HUMAN; AC: Q9E977; PRT; 759 AA.
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22	858	30.0	1906	1	AT\$2_MOUSE	AT\$2_MOUSE; AC: Q9E977; PRT; 1906 AA.
23	847	29.6	867	2	Q66QV3	AT\$2_MOUSE; AC: Q9E977; PRT; 867 AA.
24	837.5	29.3	930	1	AT\$5_MOUSE	AT\$5_MOUSE; AC: Q9E977; PRT; 930 AA.
25	830.5	29.0	928	2	Q6YI9	AT\$5_MOUSE; AC: Q9E977; PRT; 928 AA.
26	827	28.9	930	1	AT\$5_HUMAN	AT\$5_HUMAN; AC: Q9E977; PRT; 930 AA.
27	822	28.8	1935	1	AT\$9_HUMAN	AT\$9_HUMAN; AC: Q9E977; PRT; 1935 AA.
28	786	27.5	1911	1	AT\$20_HUMAN	AT\$20_HUMAN; AC: Q9E977; PRT; 1911 AA.
29	706.5	24.7	2165	2	Q1791	AT\$20_HUMAN; AC: Q9E977; PRT; 2165 AA.
30	650.5	22.8	997	1	AT\$7_HUMAN	AT\$7_HUMAN; AC: Q9E977; PRT; 997 AA.
31	649.5	22.7	1686	2	Q6P7J9	AT\$7_HUMAN; AC: Q9E977; PRT; 1686 AA.

Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

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No. Score Query

Match Length DB ID

Description

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Gapop 10.0 , Gapext 0.5

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1612378 seqs, 512079187 residues

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03;*

1: uniprot_sprot:*

2: uniprot_trembl:*

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11	1221.5	42.7	967	1	AT\$1_RAT	AT\$1_RAT; AC: Q9E977; PRT; 968 AA.
12	1220.5	42.7	957	2	Q6BET2	AT\$1_RAT; AC: Q9E977; PRT; 968 AA.
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14	1193	41.7	967	2	QBNZ6	AT\$1_HUMAN; AC: Q9E977; PRT; 968 AA.
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17	1084	37.9	203	2	Q8CBH0	AT\$1_MOUSE; AC: Q9E977; PRT; 203 AA.
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25	830.5	29.0	928	2	Q6YI9	AT\$5_MOUSE; AC: Q9E977; PRT; 928 AA.
26	827	28.9	930	1	AT\$5_HUMAN	AT\$5_HUMAN; AC: Q9E977; PRT; 930 AA.
27	822	28.8	1935	1	AT\$9_HUMAN	AT\$9_HUMAN; AC: Q9E977; PRT; 1935 AA.
28	786	27.5	1911	1	AT\$20_HUMAN	AT\$20_HUMAN; AC: Q9E977; PRT; 1911 AA.
29	706.5	24.7	2165	2	Q1791	AT\$20_HUMAN; AC: Q9E977; PRT; 2165 AA.
30	650.5	22.8	997	1	AT\$7_HUMAN	AT\$7_HUMAN; AC: Q9E977; PRT; 997 AA.
31	649					

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:19:43 ; Search time 41 Seconds

Title: US-10-628-432-32

Perfect score: 2859

Sequence: I MSQTGSHPGRLAGRWLWGA.....DQLQDENIPOQAVDYKDDDK 529

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Listing first 45 summaries

Database : PIR_79;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

No.	Score	Query	Match	Length	DB	ID	Description
1	2801	98.0	837	2	T00355		hypothetical protein KIAA0688 - human
2	1222	42.7	951	2	T00017		C-Species: Homo sapiens (man)
3	706.5	24.7	2165	2	T21371		C-Accesion: T00355
4	479.5	16.8	1205	2	T18157		R;Bniihawa, K.; Nagase, T.; Suyama, M.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N
5	436.5	15.3	550	2	T47158		DNA Res. 5, 169-176, 1998
6	277.5	9.7	860	2	T16892		A-Title: Prediction of the coding sequences of unidentified human genes. X. The comple
7	277.5	9.7	1444	2	T18856		A-Reference number: 214142; MUID:98403880; PMID:9734811
8	268.5	9.4	903	2	S60257		A>Status: preliminary; translated from GB/EMBL/DDBJ
9	250	8.7	480	1	A30065		A-Molecule type: mRNA
10	236.5	8.3	802	2	S66260		A-Residues: 1-837 <ISH>
11	234	8.2	609	2	S55270		A-Cross-references: UNIPROT:075173; EMBL:AB014588; NID:93327189; PIDN:BAA31663.1; PID:9
12	231.5	8.1	814	2	G02390		A-Experimental source: brain
13	230	8.0	478	2	A43296		C-Genetics:
14	227.5	8.0	478	2	JQ1301		A;Gene: KIAA0688
15	225.5	7.9	571	2	S24789		P;519-575;/Domain: thrombospondin type 1 repeat homology <THS3>
16	224	7.8	615	2	A55796		Query Match 98.0%; Score 2801; DB 2; Length 837;
17	221.5	7.7	478	2	JC4880		Best Local Similarity 99.6%; Pred. No. 3.9e-200; Matches 518; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
18	221	7.7	481	2	JC4342		Qy 1 MSQTGSHPGRLAGRWLWGA.....DQLQDENIPOQAVDYKDDDK 529 Db 1 MSQTGSHPGRLAGRWLWGA.....DQLQDENIPOQAVDYKDDDK 529
19	218.5	7.6	549	2	S48169		Qy 61 IVFPEKLNGSLTULPGSAPPALCRLCQAFGETLLESDQSCVQEGLTQVLQGQPLLG 120 Db 61 IVFPEKLNGSLTULPGSAPPALCRLCQAFGETLLESDQSCVQEGLTQVLQGQPLLG 120
20	217.5	7.6	419	2	S41607		Db 61 IVFPEKLNGSLTULPGSAPPALCRLCQAFGETLLESDQSCVQEGLTQVLQGQPLLG 120
21	217	7.6	481	2	S43125		Qy 181 LRRKSPASQGPCKMCVKAFLPGLSPSPRPRKRFASLSRIFVETLVADDKMAAFHAGLIR Db 181 LRRKSPASQGPCKMCVKAFLPGLSPSPRPRKRFASLSRIFVETLVADDKMAAFHAGLIR
22	214.5	7.5	617	2	S48160		Qy 241 YLLTWNAAAKAFKHPSTRNPVSLVTVLVLGSGEFGQVGSQAQTFRPCWQGIN 300 Db 241 YLLTWNAAAKAFKHPSTRNPVSLVTVLVLGSGEFGQVGSQAQTFRPCWQGIN 300
23	214	7.5	411	1	HYSNPA		Db 301 TPEDSPDPDFDTAILPQDLCGVSTCDLGMADVGTVCDPAPSCATVBDGQSAFTTA 360
24	211.5	7.4	414	2	S4109		Db 301 TPEDSPDPDFDTAILPQDLCGVSTCDLGMADVGTVCDPAPSCATVBDGQSAFTTA 360
25	210.5	7.4	508	2	T22836		Qy 361 HQLGVFVNLDHNSKPCISLNGLSTERHVMAPVMARYDEPESWPSARFIDFLDNGY 420 Db 361 HELGHVFVNLDHNSKPCISLNGLSTERHVMAPVMARYDEPESWPSARFIDFLDNGY 420
26	210	7.3	826	2	A60385		
27	207.5	7.3	484	2	JC8920		
28	200	7.0	610	2	JC7530		
29	199.5						

atrypsin B (EC 3.4.24.29) - Glucuronidase - Glucuronyl
disintegrin and metalloprotease-disintegrin and me-
talloprotease-disintegrin-like m
hypothetical Prote-
disintegrin-like m
androgen-regulated
metalloprotease
disintegrin-like m
metalloprotease
fertilin alpha-1 -
hemorrhagic factor
metalloprotease
fertilin alpha-II
hemorrhagic protei

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: November 3, 2005, 08:20:33 ; Search time 42 Seconds
(without alignments)
940.223 Million cell updates/sec

Title: US-10-628-432-32

Perfect score: 2859

Sequence: 1 MSQGSHPGRGLAGRWLWGA.....DQLQDFNIPQAVDYKDDDK 529

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
Issued Patents AA:
1: /cggn2_6/ptodata/1/iaa/5A_COMB.pep: *
2: /cggn2_6/prodata/1/iaa/5B_COMB.pep: *
3: /cggn2_6/prodata/1/iaa/6A_COMB.pep: *
4: /cggn2_6/prodata/1/iaa/6B_COMB.pep: *
5: /cggn2_6/prodata/1/iaa/PCTR5_COMB.pep: *
6: /cggn2_6/prodata/1/iaa/backfile1.pep: *

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SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	2805	98.1	837	4 US-09-122-126B-2
2	2805	98.1	837	4 US-09-634-286A-2
3	2805	98.1	837	4 US-10-247-685-2
4	1222	950	4	US-09-321-987B-4
5	1193	41.7	967	4 US-09-130-491-2
6	1189	41.6	949	4 US-09-568-559-2
7	1097	38.4	950	4 US-10-009-332-1
8	1050	36.7	727	4 US-09-442-023-12
9	1046.5	36.6	727	4 US-09-45-023A-1
10	1011.5	35.4	905	3 US-09-369-364A-9
11	852.5	29.8	608	4 US-09-130-491-13
12	837.5	29.3	930	3 US-09-369-364A-2
13	827	28.9	930	4 US-09-122-126B-15
14	827	28.9	930	4 US-09-634-286A-15
15	827	28.9	930	4 US-10-247-685-15
16	783.5	27.4	1882	3 US-09-369-364A-13
17	733	25.6	874	4 US-09-369-364A-15
18	717	25.1	2150	4 US-09-221-987B-2
19	706.5	24.7	2165	4 US-09-800-728-155
20	645.5	22.6	997	3 US-09-369-364A-7
21	636	22.2	245	3 US-09-369-364A-11
22	592	20.7	589	4 US-09-963-791-12
23	592	20.7	908	4 US-09-963-791-2
24	574	20.1	1104	4 US-09-981-953A-4
25	559.5	19.6	438	4 US-09-963-791-22
26	559.5	18.6	757	4 US-09-963-791-24
27	544.5	19.0	507	4 US-09-963-791-10

ALIGNMENTS

RESULT 1
US-09-122-126B-2
; Sequence 2, Appli
; Patent No. 6451575
; GENERAL INFORMATION
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: AGGRECAN DEGRADING METALLO PROTEASES
; FILE REFERENCE: DM6909
; CURRENT APPLICATION NUMBER: US/09-122-126B
; CURRENT FILING DATE: 1998-07-24
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-122-126B-2

Query Match Similarity 98.1%; Score 2805; DB 4; Length 837;
Best Local Matches 519; Conservative 99.8%; Pred. No. 2.1e-245; Indels 0; Gaps 0;

QY 1 MSQGSHPGRGLAGRWLWGAQPCLLPIPLSWIPLLILLASLLPSRLASPLPREE 60
Db 1 MSQGSHPGRGLAGRWLWGAQPCLLPIPLSWIPLLILLASLLPSRLASPLPREE 60

QY 61 IVFPEKLNSVVLPGSGAPRLQPLQACETULLLEQDSGVQVQEGLTQYLGPQELIG 120
Db 61 IVFPEKLNSVVLPGSGAPRLCRLQARFCETULLLEQDSGVQVQEGLTQYLGPQELIG 120

QY 121 GASPGTYLGTGTDPSVAVSLWWDGGALLGVQYRGAVBLHOPLEGGTNPNSAGGPAGII 180
Db 121 GASPGTYLGTGTDPSVAVSLWWDGGALLGVQYRGAVBLHOPLEGGTNPNSAGGPAGII 180

QY 181 LIRKSPASGGQPMCNVAKLGSSSPRPRAKEFASLSRFVETLWADDKMAAFHGAGLKR 240
Db 181 LIRKSPASGGQPMCNVAKLGSSSPRPRAKEFASLSRFVETLWADDKMAAFHGAGLKR 240

QY 241 YLTVMAAKAKFHRSPRIRNPVSLUVTRVLTGSGEGPQVPSAQTLRSCAWORGII 300
Db 241 YLTVMAAKAKFHRSPRIRNPVSLUVTRVLTGSGEGPQVPSAQTLRSCAWORGII 300

QY 301 TPEDSDPFHDPAITLFRDQLGVSTCDLGHADVGTVCPDARSCTA VEDDGQSAFTAA 360
Db 301 TPEDSDPFHDPAITLFRDQLGVSTCDLGHADVGTVCPDARSCTA VEDDGQSAFTAA 360

QY 361 HQLGHVFMHDNSKCIISLNGPLSLSRHMRAVPMVHVDPEPWSCSAFETDFLDNY 420
Db 361 HQLGHVFMHDNSKCIISLNGPLSLSRHMRAVPMVHVDPEPWSCSAFETDFLDNY 420

QY 361 HELGHVFMHDNSKCIISLNGPLSLSRHMRAVPMVHVDPEPWSCSAFETDFLDNY 420

